

IN THE SPECIFICATION:

Please replace the Substitute Sequence Listing filed on or about March 28, 2007 with the instant Substitute Sequence Listing filed herewith. Accordingly, please insert the Substitute Sequence Listing filed herewith into the Application at the end of the Specification.

Please amend the paragraphs identified below as follows:

[0061] Figs. 1A and 1B show cellular proliferation on different solid media and sequence alignments of different members of the MazF family of RNA Interferases. Fig. 1A shows growth properties of *E. coli* BW25113(Δ araBAD) cells transformed with pBAD-MazF, pBAD-MazF R29S or pBAD-MazF R86G plasmid, respectively. Fig. 1B depicts sequence alignments of MazF of *Escherichia coli* (GenBank Accession No. NP_289336.1; SEQ ID NO: 2) with that of *Bacillus halodurans* (GenBank Accession No. NP_244588.1; SEQ ID NO: 46), *Staphylococcus epidermidis* (GenBank Accession No. AAG23809.1; SEQ ID NO: 47), *Staphylococcus aureus* (GenBank Accession No. NP_372592.1; SEQ ID NO: 48), *Bacillus subtilis* (GenBank Accession No. 1NE8_A; SEQ ID NO: 49), *Neisseria meningitides* (GenBank Accession No. NP_266040.1; SEQ ID NO: 50), *Morganella morganii* (GenBank Accession No. AAC82516.1; SEQ ID NO: 51) and *Mycobacterium tuberculosis* (GenBank Accession No. NP_217317.1; SEQ ID NO: 52).

[0075] Fig. 15 shows alignments of the amino acid sequences of MazE homologs. Sequence alignments of eight MazE family proteins are shown. The amino acid sequences shown therein (as presented from top to bottom) are designated SEQ ID NO: 60; SEQ ID NO: 61; SEQ ID NO: 62; SEQ ID NO: 63; SEQ ID NO: 64; SEQ ID NO: 65; and SEQ ID NO: 66.

[0080] **Figs. 20A and 20B** show a nucleic (SEQ ID NO: 1) and amino acid (SEQ ID NO: 2) sequence of *E. coli* MazF.

[0081] **Figs. 21A and 21B** show a nucleic (SEQ ID NO: 5) and amino acid (SEQ ID NO: 6) sequence of *E. coli* MazE.

[0088] **Figs. 28A-E** show a photograph of a polyacrylamide gel (A) or autoradiograms of polyacrylamide gels (B-E) that illustrate PemK mediated endoribonuclease activity. The RNA sequences complementary to the DNA sequence ladders around the PemK(His)₆ cleavage sites are shown at the right-hand side and are designated SEQ ID NO: 93 (Fig. 28B); SEQ ID NO: 94 (Fig. 28C); SEQ ID NO: 95 (Fig. 28D); and SEQ ID NO: 96 (Fig. 28E).

[0089] **Figs. 29A-B** show a photograph of a polyacrylamide sequencing gel (A) and an autoradiogram of a polyacrylamide gel (B) that reveal the specificity of PemK mediated endoribonuclease activity for single stranded RNA. The RNA sequence shown therein is designated SEQ ID NO: 97.

[0090] **Figs. 30A-D** show a Northern blot analysis (A) or autoradiograms of polyacrylamide gels (B-D) that depict PemK mediated endonucleolytic activity on various mRNAs *in vivo*. The RNA sequences shown therein are designated SEQ ID NO: 94 (Fig. 30B); SEQ ID NO: 98 (Fig. 30C); and SEQ ID NO: 99 (Fig. 30D).

[0091] **Figs. 31A and 31B** show a nucleic (SEQ ID NO: 3) and amino acid (SEQ ID NO: 4) sequence of *E. coli* PemK.

[0092] **Figs. 32A and 32B** show a nucleic (SEQ ID NO: 7) and amino acid (SEQ ID NO: 8) sequence of *E. coli* PemI.

[0093] Fig. 33 shows sequence alignments of PemK, ChpBK and MazF polypeptides. The amino acid sequences shown therein (as presented from top to bottom) are designated SEQ ID NO: 4; SEQ ID NO: 88; and SEQ ID NO: 2.

[0094] Fig. 34 shows sequence alignments of PemK, ChpBK, MazF and three PemK-like proteins from *Mycobacterium celatum*, *Pseudomonas putida* KT2440 and *Shigella flexneri* 2a str. 301. The amino acid sequences shown therein (as presented from top to bottom) are designated SEQ ID NO: 4; SEQ ID NO: 86; SEQ ID NO: 85; SEQ ID NO: 88; SEQ ID NO: 87; and SEQ ID NO: 2.

[0099] Figs. 39A-B show (A) the amino acid sequence of the N-terminal extension of the MazF (E24A) mutant expressed with pET28a and (B) a photograph of a polyacrylamide gel showing a band corresponding to uncleaved MazF mutant fusion protein (lane 1) and thrombin cleaved MazF mutant fusion protein (lane 2). The amino acid sequence of the N-terminal extension is designated SEQ ID NO: 100.

[0100] Fig. 40 shows a primer extension analysis of MazF-*mtI* mRNA interferase activity. The RNA sequence shown therein is designated SEQ ID NO: 101.

[0101] Figs. 41A-B show sequence alignments of (A) *E. coli* MazF and its homologs in *M. tuberculosis* and (B) *E. coli* MazF and its homologs in *B. subtilis*, *B. anthracis* and *S. aureus*. The amino acid sequences shown in Fig. 41A (as presented from top to bottom) are designated SEQ ID NO: 75; SEQ ID NO: 74; SEQ ID NO: 2; SEQ ID NO: 76; SEQ ID NO: 77; and SEQ ID NO: 78. The amino acid sequences shown in Fig. 41B (as presented from top to bottom) are designated SEQ ID NO: 49; SEQ ID NO: 80; SEQ ID NO: 48; and SEQ ID NO: 2.

[0102] ~~[0101]~~ Fig. 42 shows an RNA sequence of the *mazF* open reading frame (ORF). All ACA sequences are shown in gray, and base changes that replace ACA sequences without altering the MazF amino acid sequence encoded therefrom are shown on top of the RNA

sequence. The MazF amino acid sequence shown therein is designated SEQ ID NO: 2 and the MazF RNA sequence shown therein is designated SEQ ID NO: 102.

[0352] The the *era* mRNA (from pET28a-Era) and the *lpp* mRNA (from *E. coli* chromosomal DNA, see Fig. 30D) are shown. The conserved UA dinucleotides are shown in bold. The numbers show the positions of the nucleotides in mRNA taking the A residue in the initiation codon AUG as +1.

Gene Names	Primer	mRNA sequences around the cleavage sites
<i>mazG</i>	G1	(-27) UUUUAAACUUU U AAGAAGGAGA (-8) (SEQ ID NO: 103)
		(-14) AAGGAGAU AU U A CAUAUGAAT (+6) (SEQ ID NO: 104)
	G2	(+112) GAAGAAACCU A CGAAGUGCU (+131) (SEQ ID NO: 105)
	G3	(+196) GUGGUGUUU U ACGCGCAAU (+215) (SEQ ID NO: 106)
		(+234) CUUGACUU U AAUGAUUUU (+253) (SEQ ID NO: 107)
		(+240) CUUUAAGAU U AUUUGCGCUG (+259) (SEQ ID NO: 108)
		(+290) CGCAUGUUU U GCUGAUAGUU (+309) (SEQ ID NO: 109)
	G4	(+523) GAGGUGAUG U ACGAAGCGCG (+542) (SEQ ID NO: 110)
	G5	(+597) UGCCACGGU U AAUCUGGCUC (+616) (SEQ ID NO: 111)
		(+684) AGUGGAGCG U AUUGUUGCCG (+703) (SEQ ID NO: 112)
<i>era</i>	E1	(+10) GATAAAAGU U ACUGCGGAUU (+29) (SEQ ID NO: 113)
	E2	(+144) GGGGAUCCA U ACUGAAGGCG (+163) (SEQ ID NO: 114)
		(+169) CAGGCGAUC U ACGUCGAUAC (+188) (SEQ ID NO: 115)
	E3	(+509) GUAAGCAUC U ACCUGAAGCG (+528) (SEQ ID NO: 116)
		(+541) CCGGAAGAU U ACAUCACCGA (+560) (SEQ ID NO: 117)
	E4	(+625) GAACUGCCG U AUCUCCGUGAC (+644) (SEQ ID NO: 118)
		(+676) CGCGGUGGU U AUGACAUCAA (+695) (SEQ ID NO: 119)
<i>lpp</i>	<i>lppC</i>	(+210) CAACAUGGCU U ACTAAATACC (+229) (SEQ ID NO: 120)